

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: US
- (F) ZIP: 92037
- (G) TELEPHONE: (619) 784-2937
- (H) TELEFAX: (619) 784-9399

(ii) TITLE OF INVENTION: MHC CLASS II ANTIGEN PRESENTING SYSTEMS
AND METHODS FOR ACTIVATING CD4+ T CELLS

(iii) NUMBER OF SEQUENCES: 56

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/
- (B) FILING DATE: 22-MAY-1997
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/018,175
- (B) FILING DATE: 23-MAY-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTCGATGCA CACTCACATT CTTCTCCTAA TAGGATAATA AAAC TTTCCA TGAAAAATAT	60
GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC TTAATTAAAA	120
TAGATAAATG GGAGCGGCTG GAATGGCGGA GCATGACCAA GTTCCTCCGC CAATCAGTCG	180
TAAAACAGAA GTCGTGGAAG GCGGATAGAA AGAATGTTCCG ATTTGACGGG CAAGCATGTC	240
TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT CATGACCAAG	300
AATATAGCGG TGTGAGTGAG CGGGAAGCTC GGTTCCTGTC CAGATCGAAC TCAAACTAG	360
TCCAGCCAGT CGCTGTCGAA ACTAATTAAG TTAATGAGTT TTTTCATGTA GTTTCGCGCT	420
GAGCAACAAT TAAGTTTATG TTTCAGTTTC GCTTAGATTT CGCTGAAGGA CTTGCCACTT	480
TCAATCAATA CTTTAGAACA AAATCAAAAC TCATTCTAAT AGCTTGGTGT TCATCTTTTT	540
TTTTAATGAT AAGCATTTTG TCGTTTATAC TTTTATATT TCGATATTAA ACCACCTATG	600
AAGTTCATTT TAATCGCCAG ATAAGCAATA TATTGTGTAA ATATTTGTAT TCTTTATCAG	660
GAAATTCAGG GAGACGGGGA AGTTACTATC TACTAAAAGC CAAACAATTT CTTACAGTTT	720
TACTCTCTCT ACTCTAGAGT	740

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGTTGC AGGACAGGAT GTGGTGCCCG ATGTGACTAG CTCTTTGCTG CAGGCCGTCC	60
TATCCTCTGG TTCCGATAAG AGACCCAGAA CTCGGGCCCC CCACCGCCCA CCGCCACCCC	120

CATACATATG TGGTACGCAA GTAAGAGTGC CTGCGCATGC CCCATGTGCC CCACCAAGAG 180
TTTTGCATCC CATACAAGTC CCCAAAGTGG AGAACCGAAC CAATTCTTCG CGGGCAGAAC 240
AAAAGCTTCT GCACACGTCT CCACTCGAAT TTGGAGCCGG CCGGCGTGTG CAAAAGAGGT 300
GAATCGAACG AAAGACCCGT GTGTAAAGCC GCGTTTCCAA AATGTATAAA ACCGAGAGCA 360
TCTGGCCAAT GTGCATCAGT TGTGGTCAGC AGCAAAATCA AGTGAATCAT CTCAGTGCAA 420
CTAAAGG 427

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGAATTCC ACCATGCCGT GCAGCAGAGC TCTGA 35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGGATCCT CATAAAGGCC CTGGGTGTC 29

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGAATTCC ACCATGGCTC TGCAGATCCC CA

32

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGATCCT CACTGCAGGA GCCCTGCT

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGTTGCAGG ACAGGATGTG GTGCCCCGATG TGA CTAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCC ATGTGCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TGCAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCCTGCAGA GACCTCCAG AGACCAGGAT GCCGTGCAGC AGAGCTCTGA	480
TTCTGGGGGT CCTCGCCCTG AACACCATGC TCAGCCTCTG CGGAGGTGAA GACGACATTG	540
AGGCCGACCA CGTAGGCTTC TATGGTACAA CTGTTTATCA GTCTCCTGGA GACATTGGCC	600
AGTACACACA TGAATTTGAT GGTGATGAGT TGTTCTATGT GGA CTTGAT AAGAAGAAAA	660
CTGTCTGGAG GCTTCCTGAG TTTGGCCAAT TGATACTCTT TGAGCCCCAA GGTGGACTGC	720
AAAACATAGC TGCAGAAAAA CACAATTGG GAATCTTGAC TAAGAGGTCA AATTTACCCC	780
CAGCTACCAA TGAGGCTCCT CAAGCGACTG TGTTCCCCAA GTCCCCTGTG CTGCTGGGTC	840
AGCCCAACAC CCTTATCTGC TTTGTGGACA ACATCTTCCC ACCTGTGATC AACATCAGAT	900
GGCTCAGGAA TAGCAAGTCA GTCACAGACG GCGTTTATGA GACCAGCTTC CTCGTCAACC	960
GTGACCATT CTTCCACAAG CTGTCTTATC TCACCTTCAT CCCTTCTGAT GATGACATTT	1020
ATGACTGCAA GGTGGAGCAC TGGGGCCTGG AGGAGCCGCT TCTGAAACAC TGGGAACCTG	1080
AGATTCCAGC CCCCATGTCA GAGCTGACAG AAAGTGTGGT GTGTGCCCTG GGGTTGCTCTG	1140
TGGGCCTTGT GGGCATCGTG GTGGGCACCA TCTTCATCAT TCAAGGCCTG CGATCAGGTG	1200
GCACCTCCAG ACACCCAGGG CCTTTATGAG TCACACCCCTG GAAAGGAAGG TGTGTGTCCC	1260
TCTTCATGGA AGAAGTGGTG TTCTGGGTGT CGAATTCGAG CTCGGTACCC GGGGATCCTC	1320
TAGAGTCGAC CTGCAGGCAT GCAATTCGAT GCACACTCAC ATTCTTCTCC TAATACGATA	1380
ATAAACTTT CCATGAAAAA TATGAAAAA TATATGAAAA TTGAGAAATC CAAAAAACTG	1440
ATAAACGCTC TACTTAATTA AAATAGATAA ATGGGAGCGG CAGGAATGGC GGAGCATGGC	1500
CAAGTTCCTC CGCCAATCAG TCGTAAAAA GAAGTCGTGG AAAGCGGATA GAAAGAATGT	1560
TCGATTTGAC GGGCAAGCAT GTCTGCTATG TGGCGGATTG CGGAGGAATT GCACTGGAGA	1620
CCAGCAAGGT TCTCATGACC AAGAATATAG CGGTGAGTGA GCGGGAAGCT CGGTTTCTGT	1680
CCAGATCGAA CTCAAAATA GTCCAGCCAG TCGCTGTGCA AACTAATTAA GTAAATGAGT	1740

TTTTCATGTT	AGTTTCGCGC	TGAGCAACAA	TTAAGTTTAT	GTTTCAGTTC	GGCTTAGATT	1800
TCGCTGAAGG	ACTTGCCACT	TTCAATCAAT	ACTTTAGAAC	AAAATCAAAA	CTCATTCTAA	1860
TAGCTTGGTG	TTCATCTTTT	TTTTTAATGA	TAAGCATTTT	GTGCTTTATA	CTTTTTATAT	1920
TTCGATATTA	AACCACCTAT	GAAGTTCATT	TTAATCGCCA	GATAAGCAAT	ATATTGTGTA	1980
AATATTTGTA	TTCTTTATCA	GGAAATTCAG	GGAGACGGGG	AAGTTACTAT	CTACTAAAAG	2040
CCAAACAATT	TCTTACAGTT	TTACTCTCTC	TACTCTAGAG	CTTGGCACTG	GCCGTCGTTT	2100
TACAACGTCG	TGACTGGGAA	AACCCTGGCG	TTACCCAACT	TAATCGCCTT	GCAGCACATC	2160
CCCCTTTTCG	CAGCTGGCGT	AATAGCGAAG	AGGCCCGCAC	CGATCGCCCT	TCCCAACAGT	2220
TGCGCAGCCT	GAATGGCGAA	TGGCGCCTGA	TGCGGTATTT	TCTCCTTACG	CATCTGTGCG	2280
GTATTTGACA	CCGCATATGG	TGCACTCTCA	GTACAATCTG	CTCTGATGCC	GCATAGTTAA	2340
GCCAGCCCCG	ACACCCGCCA	ACACCCGCTG	ACGCGCCCTG	ACGGGCTTGT	CTGCTCCCGG	2400
CATCCGCTTA	CAGACAAGCT	GTGACCGTCT	CCGGGAGCTG	CATGTGTCAG	AGGTTTTTCAC	2460
CGTCATCACC	GAAACGCGCG	AGACGAAAGG	GCCTCGTGAT	ACGCCTATTT	TTATAGGTTA	2520
ATGTCATGAT	AATAATGGTT	TCTTAGACGT	CAGGTGGCAC	TTTTCGGGGA	AATGTGCGCG	2580
GAACCCCTAT	TTGTTTATTT	TTCTAAATAC	ATTCAAATAT	GTATCCGCTC	ATGAGACAAT	2640
AACCCGTGATA	AATGCTTCAA	TAATATTGAA	AAAGGAAGAG	TATGAGTATT	CAACATTTCC	2700
GTGTGCGCCT	TATTCCTTTT	TTTGGCGCAT	TTTGCCTTCC	TGTTTTTGCT	CACCCAGAAA	2760
CGTGGTGAA	AGTAAAAGAT	GCTGAAGATC	AGTTGGGTGC	ACGAGTGGGT	TACATCGAAC	2820
TGGATCTCAA	CAGCGGTAAG	ATCCTTGAGA	GTTTTCGCCC	CGAAGAACGT	TTTCCAATGA	2880
TGAGCACTTT	TAAAGTTCTG	CTATGTGGCG	CGGTATTATC	CCGTATTGAC	GCCGGGCAAG	2940
AGCAACTCGG	TCGCCGCATA	CACTATTCTC	AGAATGACTT	GGTTGAGTAC	TCACCAGTCA	3000
CAGAAAAGCA	TCTTACGGAT	GGCATGACAG	TAAGAGAATT	ATGCAGTGCT	GCCATAACCA	3060
TGACTGATAA	CACTGCGGCC	AACTTACTTC	TGACAACGAT	CGGAGGACCG	AAGGAGCTAA	3120
CCGCTTTTTT	GCACAACATG	GGGGATCATG	TAACTCGCCT	TGATCGTTGG	GAACCGGAGC	3180
TGAATGAAGC	CATACCAAAC	GACGAGCGTG	ACACCAGGAT	GCCTGTAGCA	ATGGCAACAA	3240
CGTTGCGCAA	ACTATTAACT	GGCGAACTAC	TTACTCTAGC	TTCCCGGCAA	CAATTAATAG	3300
ACTGGATGGA	GGCGGATAAA	GTTGCAGGAC	CACTTCTGCG	CTCGGCCCTT	CCGGCTGGCT	3360
GGTTTATTGC	TGATAAATCT	GGAGCCGGTG	AGCGTGGGTC	TCGCGGTATC	ATTGCAGCAC	3420
TGGGGCCAGA	TGTAAGCCC	TCCCGTATCG	TAGTTATCTA	CACGACGGGG	AGTCAGGCAA	3480
CTATGGATGA	ACGAAATAGA	CAGATCGCTG	AGATAGGTGC	CTCACTGATT	AAGCATTGGT	3540
AACTGTCAGA	CCAAGTTTAC	TCATATATAC	TTTAGATTGA	TTTAAAACTT	CATTTTTAAT	3600
TTAAAAGGAT	CTAGGTGAAG	ATCCTTTTTG	ATAATCTCAT	GACCAAAATC	CCTTAACGTG	3660
AGTTTTCGTT	CCACTGAGCG	TCAGACCCCG	TAGAAAAGAT	CAAAGGATCT	TCTTGAGATC	3720
CTTTTTTTCT	GCGCGTAATC	TGCTGCTTGC	AAAGAAAAAA	ACCACCGCTA	CCAGCGGTGG	3780
TTTGTTTGCC	GGATCAAGAG	CTACCAACTC	TTTTTCCGAA	GGTAACTGGC	TTCAGCAGAG	3840
CGCAGATACC	AAATACTGTC	CTTCTAGTGT	AGCCGTAGTT	AGGCCACCAC	TTCAAGAACT	3900
CTGTAGCACC	GCCTACATAC	CTCGCTCTGC	TAATCTGTGT	ACCAGTGGCT	GCTGCCAGTG	3960
GCGATAAGTC	GTGTCTTACC	GGGTTGGACT	CAAGACGATA	GTTACCGGAT	AAGGCGCAGC	4020
GGTCGGGCTG	AACGGGGGGT	TCGTGCACAC	AGCCAGCTT	GGAGCGAACG	ACCTACACCG	4080

AACTGAGATA CCTACAGCGT GAGCATTGAG AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG	4140
CGGACAGGTA TCCGGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGAGG GAGCTTCCAG	4200
GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC	4260
GATTTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCCT	4320
TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTTATCCC	4380
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC	4440
GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGCGCCCA ATACGCAAAC	4500
CGCCTCTCCC CGCGCGTTGG CCGATTCAAT AATGCAGCTG GCACGACAGG TTTCCCGACT	4560
GGAAAGCGGG CAGTGAGCGC AACGCAATTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC	4620
AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC GGATAACAAT	4680
TTCACACAGG AAACAGCTAT GACCATGATT ACG	4713

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGTTGCAGG ACAGGATGTG GTGCCCCGATG TGA TAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCA CCGCCACCG CCACCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTGGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCCCTGCTG TGCCCTAGAG ATGGCTCTGC AGATCCCCAG CCTCCTCCTC	480
TCAGCTGCTG TGGTGGTGCT GATGGTGCTG AGCAGCCAG GGA CTGAGGG CGGAAACTCC	540
GAAAGGCATT TCGTGGTCCA GTTCAAGGGC GAGTGCTACT ACACCAACGG GACGCAGCGC	600
ATACGGCTCG TGACCAGATA CATCTACAAC CGGGAGGAGT ACGTGCGCTA CGACAGCGAC	660
GTGGGCGAGT ACCGCGCGGT GACCGAGCTG GGGCGGCCAG ACGCCGAGTA CTGGAACAGC	720

CAGCCGGAGA TCCTGGAGCG AACGCGGGCC GAGGTGGACA CGGCGTGCAG ACACAACACTAC 780
GAGGGGCGCG AGACCAGCAC CTCCCTGCGG CGGCTTGAAC AGCCCAATAT CGCCATCTCC 840
CTGTCCAGGA CAGAGGCCCT CAACCACCAC AACACTCTGG TCTGTTCCGT GACAGATTTT 900
TACCCAGCCA AGATCAAAGT GCGCTGGTTC AGGAATGGCC AGGAGGAGAC AGTGGGGGTC 960
TCATCCACAC AGCTTATTAG GAATGGGGAC TGGACCTTCC AGGTCCTGGT CATGCTGGAG 1020
ATGACCCCTC ATCAGGGAGA GGTCTACACC TGCCATGTGG AGCATCCCAG CCTGAAGAGC 1080
CCCATCACTG TGGAGTGGAG GGCACAGTCC GAGTCTGCCC GGAGCAAGAT GTTGAGCGGC 1140
ATCGGGGGCT GCGTGTCTTG GGTGATCTTC CTCGGGCTCG GCCTTTTTCAT CCGTCACAGG 1200
AGTCAGAAAG GACCTCGAGG CCCTCCTCCA GCAGGGCTCC TGCAGTGAAT CAGAGTGTTC 1260
TGACTCAGTT GACTGTCTCA GACTGTAAGA CCTACATGTC TCGAATTCGA GCTCGGTACC 1320
CGGGGATCCT CTAGAGTCGA CCTGCAGGCA TGCAATTCGA TGCACACTCA CATTCTTCTC 1380
CTAATACGAT AATAAACTT TCCATGAAAA ATATGGAAAA ATATATGAAA ATTGAGAAAT 1440
CCAAAAACT GATAAACGCT CTAATTAATT AAAATAGATA AATGGGAGCG GCAGGAATGG 1500
CGGAGCATGG CCAAGTTCCT CCGCCAATCA GTCGTAAAAC AGAAGTCGTG GAAAGCGGAT 1560
AGAAAGAATG TTCGATTGA CGGGCAAGCA TGTCTGCTAT GTGGCGGATT GCGGAGGAAT 1620
TGCAGTGGAG ACCAGGAAGG TTCTCATGAC CAAGAATATA GCGGTGAGTG AGCGGGAAGC 1680
TCGGTTTCTG TCCAGATCGA ACTCAAACT AGTCCAGCCA GTCGCTGTG AAATAATTA 1740
AGTAAATGAG TTTTTCATGT TAGTTTCGCG CTGAGCAACA ATTAAGTTTA TGTTTCAGTT 1800
CGGCTTAGAT TTCGCTGAAG GACTTGCCAC TTTCAATCAA TACTTTAGAA CAAAATCAAA 1860
ACTCATTCTA ATAGCTTGGT GTTCATCTTT TTTTAAATG ATAAGCATT TGTCGTTTAT 1920
ACTTTTTATA TTTGATATT AAACCACCTA TGAAGTTCAT TTTAATCGCC AGATAAGCAA 1980
TATATTGTGT AAATATTGT ATTCTTTATC AGGAAATTC GGGAGACGGG GAAGTTACTA 2040
TCTACTAAAA GCCAAACAAT TTCTTACAGT TTTACTCTCT CTACTCTAGA GCTTGGCACT 2100
GGCCGTCGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC TTAATCGCCT 2160
TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC 2220
TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCCTG ATGCGGTATT TTCTCCTTAC 2280
GCATCTGTGC GGTATTTTAC ACCGCATATG GTGACTCTC AGTACAATCT GCTCTGATGC 2340
CGCATAGTTA AGCCAGCCCC GACACCCGCC AACACCGGCT GACGCGCCCT GACGGGCTTG 2400
TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA 2460
GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGACGAAAG GGCCTCCTGA TACGCCTATT 2520
TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTTCGGGG 2580
AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCGGCT 2640
CATGAGACAA TAACCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT 2700
TCAACATTTT CGTGTGCCCC TTATTCCCTT TTTTGGGCA TTTTGCCCTC CTGTTTTTGC 2760
TCACCCAGAA ACGCTGGTGA AAGTAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG 2820
TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACC 2880
TTTTCCAATG ATGAGCACTT TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTATTGA 2940
CGCCGGGCAA GAGCAACTCG GTCGCCGCAT AACTATTCT CAGAATGACT TGGTTGAGTA 3000
CTCACCAGTC ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 3060

TGCCATAACC ATGAGTGATA ACACTGCGGC CAACTTACTT CTGACAACGA TCGGAGGACC 3120
GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT GTAACTCGCC TTGATCGTTG 3180
GGAACCGGAG CTGAATGAAG CCATACCAAA CGACGAGCGT GACACCACGA TGCCTGTAGC 3240
AATGGCAACA ACGTTGCGCA AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA 3300
ACAATTAATA GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT 3360
TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT CTCGCGGTAT 3420
CATTGCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC GTAGTTATCT ACACGACGGG 3480
GAGTCAGGCA ACTATGGATG AACGAAATAG ACAGATCGCT GAGATAGGTG CCTCACTGAT 3540
TAAGCATTGG TAACTGTCAG ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT 3600
TCATTTTTAA TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT 3660
CCCTTAACGT GAGTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA TCAAAGGATC 3720
TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACAAAAA AACCACCGCT 3780
ACCAGCGGTG GTTTGTTTGC CGGATCAAGA GCTACCAACT CTTTTTCCGA AGGTAAGTGG 3840
CTTCAGCAGA GCGCAGATAC CAAATACTGT CTTTCTAGTG TAGCCGTAGT TAGGCCACCA 3900
CTTCAAGAAC TCTGTAGCAC CGCCTACATA CCTCGTCTG CTAATCCTGT TACCACTGGC 3960
TGCTGCCAGT GGGGATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT AGTTACCGGA 4020
TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCTGTCACA CAGCCCAGCT TGGAGCGAAC 4080
GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA GAAAGCGCCA CGCTTCCCGA 4140
AGGGAGAAAG GCGGACAGGT ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG 4200
GGAGCTTCCA GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 4260
ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG 4320
CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTTCTTTCC 4380
TGCGTTATCC CCTGATTCTG TGGATAACCG TATTACCGCC TTTGAGTGAG CTGATACCGC 4440
TCGCGCAGC CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC 4500
AATACGCAAA CCGCCTCTCC CCGCGCGTTG GCCGATTCAT TAATGCAGCT GGCACGACAG 4560
GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT AGCTCACTCA 4620
TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG 4680
CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACG 4724

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCATGGC CATTAGTGGA GTC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGGATCCT TACAGAGGCC CCCTGCGTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACCATGGT GTGTCTGAGG CTCC

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGGATCCT CAGCTCAGGA ATCCTCTTG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCACCATGGT CCTAAACAAA GCTCTGAT

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGGATCCT CACAAGGGCC CTTGGTGTCT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCATGGC TTGAAGAAG GCCTTT

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTAGATCTC AGTGCAGAAG CCCTTT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACCATGGG CCCTGAAGAC AGAAT

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGGATCCT CACAGGGTCC CCTGGGC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACCATGGT TCTGCAGGTT TCTGCG

26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGGATCCT TATGCAGATC CTCGTTGAA

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGAATTCAC TAGAGGCTAG AGCCAT

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGGATCCTC ACAGGGTGAC TTGACC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2580 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGGTTGCAGG ACAGGATGTG GTGCCCCGATG TGACTAGCTC TTTGCTGCAG GCGGTCTCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGGG GCAGAACAAA	240
AGCTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCGATCTAG AGGCTAGAGC CATGGATGAC CAACGCGACC TCATCTCTAA	480
CCATGAGCAA TTGCCATAC TGGGCAACCG CCCTAGAGAG CCAGAAAGGT GCAGCCGTGG	540
AGCTCTGTAC ACCGGTGTTT CTGTCTGGT GGCTCTGCTC TTGGCTGGGC AGGCCACCAC	600
TGCTTACTTC CTGTACCAGC AACAGGGCCG CCTAGACAAG CTGACCATCA CCTCCCAGAA	660
CCTGCAACTG GAGAGCCTTC GCATGAAGCT TCGGAAATCT GCCAAACCTG TGAGCCAGAT	720
GCGGATGGCT ACTCCCTTGC TGATGCGTCC AATGTCCATG GATAACATGC TCCTTGGGCC	780
TGTGAAGAAC GTTACCAAGT ACGGCAACAT GACCCAGGAC CATGTGATGC ATCTGCTCAC	840
GAGGTCTGGA CCCCTGGAGT ACCCGCAGCT GAAGGGGACC TTCCCAGAGA ATCTGAAGCA	900
TCTTAAGAAC TCCATGGATG GCGTGAAGT GAAGATCTTC GAGAGCTGGA TGAAGCAGTG	960
GCTCTTGTTT GAGATGAGCA AGAACTCCCT GGAGGAGAAG AAGCCCACAG AGGCTCCACC	1020
TAAAGAGCCA CTGGACATGG AAGACCTATC TTCTGGCCTG GGAGTGACCA GGCAGGAACT	1080
GGGTCAAGTC ACCCTGTGAA GACAGAGGCC AGCATCAAGC TTATCGATAC CGTCGACCTG	1140
CAGGCATGCA ATTCGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAACTTTCCA	1200
TGAAAAATAT GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC	1260
TTAATTAAAA TAGATAAATG GGAGCGGCAG GAATGGCGGA GCATGGCCAA GTTCCTCCGC	1320
CAATCAGTCG TAAACAGAA GTCGTGAAA GCGGATAGAA AGAATGTTG ATTTGACGGG	1380
CAAGCATGTC TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGTTCT	1440
CATGACCAAG AATATAGCGG TGAGTGAGCG GGAAGCTCGG TTTCTGTCCA GATCGAACTC	1500
AAACTAGTC CAGCCAGTCG CTGTCGAAAC TAATTAAGTA AATGAGTTTT TCATGTTAGT	1560
TTCCGCTGA GCAACAATTA AGTTTATGTT TCAGTTCGGC TTAGATTTG CTGAAGGACT	1620
TGCCACTTTC AATCAATACT TTAGAACAAA ATCAAACTC ATTCTAATAG CTTGGTGTTT	1680
ATCTTTTTTT TTAATGATAA GCATTTTGTG GTTTATACTT TTTATATTTG GATATTAAAC	1740
CACCTATGAA GTTCATTTTA ATCGCCAGAT AAGCAATATA TTGTGTAAAT ATTTGTATTC	1800
TTTATCAGGA AATTCAGGGA GACGGGGAAG TTAATATCTA CTAAAAGCCA AACAATTTCT	1860
TACAGTTTTA CTCTCTCTAC TCTAGAGCTT GGCAGTGGCC GTCGTTTTAC AACGTCGTGA	1920
CTGGGAAAAC CCTGGCGTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG	1980
CTGGCGTAAT AGCGAAGAGG CCCGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA	2040
TGGCGAATGG CGCCTGATGC GGTATTTTCT CTTACGCAT CTGTGCGGTA TTTCACACCG	2100

CATATGGTGC	ACTCTCAGTA	CAATCTGCTC	TGATGCCGCA	TAGTTAAGCC	AGCCCCGACA	2160
CCCCCAACA	CCCGCTGACG	CGCCCTGACG	GGCTTGTCTG	CTCCCGGCAT	CCGCTTACAG	2220
ACAAGCTGTG	ACCGTCTCCG	GGAGCTGCAT	GTGTCAGAGG	TTTTCACCGT	CATCACCGAA	2280
ACGCGCGAGA	CGAAAGGGCC	TCGTGATACG	CCTATTTTTA	TAGGTTAATG	TCATGATAAT	2340
AATGGTTTCT	TAGACGTCAG	GTGGCACTTT	TCGGGGAAAT	GTGCGCGGAA	CCCCTATTTG	2400
TTTATTTTTC	TAAATACATT	CAAATATGTA	TCCGCTCATG	AGACAATAAC	CCTGATAAAT	2460
GCTTCAATAA	TATTGAAAAA	GGAAGAGTAT	GAGTATTCAA	CATTTCCGTG	TCGCCCTTAT	2520
TCCCTTTTTT	GCGGCATTTT	GCCTTCCTGT	TTTTGCTCAC	CCAGAAACGC	TGGTGAAAGT	2580

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGAATTCAC CATGGATGAT CAGCGCGACC TT

32

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAGGATCCT CACATGGGGA CTGGGCCAG A

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACCATGGG TCATGAACAG AACCA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGTGACT CAGTCACCTG AGCAAGG

27

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAACCATGGT CTCATTCCTG CC

22

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTCGACC TAGGAAATGT GCCATCC

27

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTAGAATTC ACCATGGCTT CAACCCGTGC CAAG

34

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTAGTCGAC TCAGGGAGGT GGGGCTTGTC C

31

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCTTGAAT TCATGGCTCC CAGCAGCCCC CGGCCC

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATTACCGGAT CCTCAGGGAG GCGTGGCTTG TGTGTTCCG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGGTACCCG TGGAGACTGC CAGAGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTGGATCCC TATGGCCGGA AGGCCTG

27

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAATTCCT GTCAGAAATGG CCACCAT

27

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTAGATCTT CACTCAGCTC TGGACGGT

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCCTTGAGC TCATGGTTGC TGGGAGCGAC GCGGGG

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATTACCGGAT CCTTAAAGAA CATTATATA CAGCACAATA CA

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTAGAATTC ACCATGGCTT GCAATTGTCA GTTG

34

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTAGTCGAC CTAAAGGAAG ACGGTCTGTT C

31

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCCTTGAAT CCATGGGCCA CACACGGAGG CAG

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATTACCGGAT CCTTATACAG GCGGTACACT TTCCTTCT

39

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTAGAATTC ACCATGGACC CCAGATGCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTTAGTCGAC TCACTCTGCA TTTGGTTTTG CTGA

34

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCCTTGAGC TCATGGATCC CCAGTGCACT ATG

33

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTACCCCGG GGTAAAAAC ATGTATCACT TTTGTGGCAT GA

42

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGGATCCA CCATGCAGCA GCCCTTCAAT T

31

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTGATCCT TAGAGCTTAT ATAAGCCGA

29

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAGAATTCTG GTACCATGCC GGAGGAGGGT TCGG

34

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTGGATCCT CAGGGGCGCA CCCACTGCA

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile	Ser	Gln	Ala	Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly
1				5					10					15	

Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Thr Ile Ala Thr Asp Glu Glu Ala Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe	Val	Arg	Phe	Asp	Ser	Asp	Ala	Ala	Ser	Gln	Arg	Met
1				5						10		